

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Chatterjee, Malaya  
Foon, Kenneth A.  
Chatterjee, Sunil K.

(ii) TITLE OF INVENTION: MURINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY 11D10  
AND METHODS OF USE THEREOF

(iii) NUMBER OF SEQUENCES: 58

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: PALO ALTO  
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(E) COUNTRY: USA  
(F) ZIP: 94304-1018

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Polizzi, Catherine M.  
(B) REGISTRATION NUMBER: 40,130  
(C) REFERENCE/DOCKET NUMBER: 30414-20003.21

(ix) TELECOMMUNICATION INFORMATION:

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(C) TELEX: 706141

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 435 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

96221-05299000  
0006350-121296

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..435

(ix) FEATURE:  
(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5

ATG GGG GCC CCT GCT CAG ATT CTT GGG TTC TTG TTG CTC TTG TTT CCA 48  
Met Gly Ala Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Phe Pro  
-20 -15 -10 -5

GGT ACC AGA TGT GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC TTA TCT 96  
Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser  
1 5 10

GCC TCT CTG GGA CAA AGA GTC AGT CTC ACT TGT CGG GCA AGT CAG GAC 144  
Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp  
15 20 25

ATT GGT ATT AAC TTA CAT TGG CTT CAG CAG GAA CCA GAT GGA ACT ATT 192  
Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile  
30 35 40

AAA CGC CTG ATC TAC GCC ACA TCC AGT TTA GGT TCT GGT GTC CCC AAA 240  
Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys  
45 50 55 60

AGG TTC AGT GGC AGT AGG TCT GGG TCA GAT TAT TCT CTC ACC ATC AGC 288  
Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser  
65 70 75

AGC CTT GAG TCT GAA GAT TTT GTA GCC TAT TAC TGT CTA CAA TAT GCT 336  
Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala  
80 85 90

AGT TCT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG 384  
Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg  
95 100 105

GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT AAG CTT 432  
Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys Leu  
110 115 120

GGG 435  
Gly  
125

25

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Ala Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Phe Pro  
 -20 -15 -10 -5

Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser  
 1 5 10

Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp  
 15 20 25

Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile  
 30 35 40

Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys  
 45 50 55 60

Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser  
 65 70 75

15 Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala  
 80 85 90

Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg  
 95 100 105

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys Leu  
 110 115 120

20 Gly  
 125

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..459

(ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

5

ATG GAA TGC AGC TGG GTC TTT CTC TTC CTC CTG TCA ATA ACT ACA GGT 48  
 Met Glu Cys Ser Trp Val Phe Leu Phe Leu Leu Ser Ile Thr Thr Gly  
 -19 -15 -10 -5

GTC CAC TCC CAG GCT TAT CTA CAG CAG TCT GGG GCT GAG CTG GTG AGG 96  
 Val His Ser Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg  
 1 5 10

TCT GGG GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTG 144  
 Ser Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Leu  
 15 20 25

ACC AGT TAC AAT ATG CAC TGG GTA AAG CAG ACA CCT GGA CAG GGC CTG 192  
 Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu  
 30 35 40 45

GAA TGG ATT GGA AAT ATT TTT CCT GGA AAT GGT GAT ACT TAC TAC AAT 240  
 Glu Trp Ile Gly Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn  
 50 55 60

CAG AAG TTT AAG GGC AAG GCC TCA TTG ACT GCA GAC ACA TCC TCC AGC 288  
 Gln Lys Phe Lys Gly Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Ser  
 65 70 75

ACA GCC TAC ATG CAG ATC AGC AGC CTG ACA TCT GAA GAC TCT GCG GTC 336  
 Thr Ala Tyr Met Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val  
 80 85 90

TAT TTC TGT GCA AGA GGG AAC TGG GAG GGT GCT CTG GAC TAC TGG GGT 384  
 Tyr Phe Cys Ala Arg Gly Asn Trp Glu Gly Ala Leu Asp Tyr Trp Gly  
 95 100 105

CAA GGA ACC TCA GTC ACC GTC TCC TCA GCC AAA ACG ACA CCC CCA CCC 432  
 Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro  
 110 115 120 125

GTC TAT CCA CTG GTC CCT GGA AGC TTG GG 461  
 Val Tyr Pro Leu Val Pro Gly Ser Leu  
 130

25

96221-05299796

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu Cys Ser Trp Val Phe Leu Phe Leu Leu Ser Ile Thr Thr Gly  
 -19 -15 -10 -5

Val His Ser Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg  
 1 5 10

Ser Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Leu  
 15 20 25

Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu  
 30 35 40 45

Glu Trp Ile Gly Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn  
 50 55 60

Gln Lys Phe Lys Gly Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Ser  
 65 70 75

15 Thr Ala Tyr Met Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val  
 80 85 90

Tyr Phe Cys Ala Arg Gly Asn Trp Glu Gly Ala Leu Asp Tyr Trp Gly  
 95 100 105

Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro  
 110 115 120 125

20 Val Tyr Pro Leu Val Pro Gly Ser Leu  
 130

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT

60

CTCACTTGTC GGGCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA 120  
GATGGAACCTA TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTGCCCCAAA 180  
AGGTTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT 240  
GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTACAC GTTCGGAGGG 300  
GGGACCAAGC TGGAAATAAA A 321

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GANATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT 60  
CTCACTTGTC GGGCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA 120  
GATGGAACCTT TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCCCCAAA 180  
AGGTTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT 240  
GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT GTCCGTACAC GTTCGGAGGG 300  
GGGACCAAGC TGGAAATAAA A 321

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT 60  
CTCACTTGTC GGGCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA 120  
GATGGAACCTA TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCCCCAAA 180  
AGGTTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT 240  
GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTGGAC GTTCGGTGGA 300  
GGCACCAAGC TGGAAATCAA A 321

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT 60  
CTCACTTGTC GGCCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA 120  
GATGGAAC TA TAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCCCCAAA 180  
AGGTTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT 240  
GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTGGAC GTTCGGTGGA 300  
GGCACCAAGC TGGAAATCAA A 321

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT 60  
CTCACTTGTC GGCCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA 120  
GATGGAAC TA TAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCCCCAAA 180  
20 AGGTTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT 240  
GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTGGAC GTTCGGTGGA 300  
GGCACCAAGC TGGAAATCAA A 321

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCCAGATGA CCCAGTCTCC ATCCTCCTTA TCTGCCTCTC TGGGAGAAAG AGTCAGTCTC 60  
ACTTGTCTGGG CAAGTCAGGA CATTGGTAGT AGCTTAAACT GGCTTCAGCA GGAACCAGAC 120  
GGAACTATTA AACGCCTGAT CTACGCCACA TCCAGTTTAG ATTCTGGTGT CCCCAAAAGG 180  
TTCAGTGGCA GTAGGTCTGG GTCAGATTAT TCTCTCACCA TCAGCAGCCT TGAGTCTGAA 240  
GATTTTGTAG ACTATTACTG TCTACAATAT GCTAGTTCTC CGTGGACGTT CGGTGGAGGC 300  
ACCAAGCTGG AAATCAAA 318

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCTCCATCCT CCTTATCTGC CTCTCTGGGA GAAAGAGTCA GTCTCACTTG TCGGGCAAGT 60  
CAGGACATTG GTAGTAGCTT AACTGGCTT CAGCAGGAAC CAGATGGAAC TATTAAACGC 120  
CTGATCTACG CCACATCCAG TTTAGATTCT GGTGTCCCCA AAAGGTTTCAG TGGCAGTAGG 180  
TCTGGGTCAG ATTATTCTCT CACCATCAGC AGCCTTGAGT CTGAAGATTT TGTAGACTAT 240  
TACTGTCTAC AATATGCTAG TTCTCCGTAC ACGTTCGGAG GGGGGACCAA GCTGNAAATA 300  
AAA 303

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT 60  
CTCACTTGTC GGGCAAGTCA GGAAATTAGT GGTTACTTAA GCTGGCTTCA GCAGAAACCA 120  
GATGGAAC TAACGCCT GATCTACAGC ACATCCACTT TAAATTCTGG TGTCCCAAAA 180  
AGGTTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT 240



GAAGATTTTG CAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTACAC GTTCGGAGGG 300  
GGGACCAAAC TGGAAATAAA A 321

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TCTCCATCCT CTTATCTGC CTCTCTGGGA GAAAGAGTCA GTCTCACTTG TCGGGCAAGT 60  
CAGGACATTG GTAATAGCTT AAAGTGGCTT CAGCAGGAAC CAGATGGAAC TATTAAACGC 120  
CTGATCTACG CCACATCCAG TTTAGATTCT GGTGTCCCCA AAAGGTTTCAG TGGCAGTAGG 180  
TCTGGGTCAG ATTATTCTCT CACCATCAGC AGCCTTGAAT CTGAAGATTT TGTAGTCTAT 240  
TACTGTCTAC AATATGCTAG TTATACGTAC ACGTTCGGAG GGGGGACCAA GTTGGAAC TA 300  
AAA 303

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT 60  
CTCACTTGTC GGGCAAGTCA GGAAATTAGT GGTTACTTAA GCTGGCTTCA GCAGAAACCA 120  
GATGGAAC TA TAAACGCCT GATCTACGCC GCATCCACTT TAGATTCTGG TGTCCCAAAA 180  
AGGTTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT 240  
GAAGATTTTG CAGACTATTA CTGTCTACAA TATCTTAGTT ATCCGCTCAC GTTCGGTGCT 300  
GGGACCAAGC TGGAGCTGAA A 321

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

5 CAGGCTTATN TACAGCAGTC TGGGGCTGAG CTGGTGAGGC CTGGGGCCTC AGTGAAGATG 60  
TCCTGCAAGG CTTCTGGCTA CACATTTACC AGTTACAATA TGCACTGGGT AAAGCAGACA 120  
CCTAGACAGG GCCTGGAATG GATTGGAGCT ATTTATCCAG GAAATGGTGA TACTTCCTAC 180  
AATCAGAAGT TCAAGGGCAA GGCCCACTG ACTGTAGACA AATCCTCCAG CACAGCCTAC 240  
ATGCAGCTCA GCAGCCTGAC ATCTGAAGAC TCTGCGGTCT ATTTCTGTGC AAGA 294

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

10 TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA 46

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

20 CAGGCTTATG TACAGCAGTC TGGGGCTGAG CTGGTGAGGC CTGGGGCCTC AGTGAAGATG 60  
TCCTGCAAGG CTTCTGGCTA CAGATTTACC AGTTACAATA TGCACTGGGT AAAGCAGACA 120  
CGTAGACAGG GCCTGGAATG GATTGGAGCA ATTTATCCAG GAAATGGTGA TACTTCCTAT 180  
AATCAGAAGT TCAAGGGCAA GGCCCACTG ATTGTAGACA AATCCTCCAG CACAGCCTAC 240  
ATGCAGCTCA GCAGCCTGAC ATCTGAAGAC TCTGCGGTCT ATTTCTGTGC AAGAGAGAGG 300  
25 GGTAACCTACG TAGGACATAT GGACTACTGG GGTCAAGGAA CCTCAGTCAC CGTCTCCTCA 360

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

5 CAGGCTTATC TACAGCAGTC TGGGGCTGAG CTGGTAAGGC CTGGGTCCTC AGTGAAGATG 60  
TCCTGCAAGG CTTCTGGCTA CACATTTACC AGTTACAATA TGCACTGGGT AAAGCAGACA 120  
CCTAGACAGG GCCTGGAATG GATTGGAGCT ATTTATCCAG GAAATGGTGA TACTTCCTAC 180  
AATCAGAAGT TCAAGGGCAA GGCCCACTG ACTGTAGACA AATCCTCCAG CACAGCCTAC 240  
ATGCAGCTCA GCAGCCTGAC ATCTGAAGAC TCTGCGGTCT ATTTCTGTGC AAGAGGGGAT 300  
TACTCCGGTA GTATAGACTA CTGGGGCCAA GGCACCACTC TCACAGTCTC CTCA 354

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

15 CAGGCTTATC TACAGCAGTC TGGGGCTGAG CTGGTGAGGC CTGGGGCCTC AGTGAAGATG 60  
TCCTGCAAGG CTTCTGGCTA CACATTTACC AGTTACAATA TGCACTGGGT AAAGCAGACA 120  
CCTAGACAGG GCCTGGAATG GATTGGAGCT ATTTATCCAG GAAATGGTGA TACTTCCTAC 180  
AATCAGAAGT TCAAGGGCAA GGCCCACTG ACTGTAGACA AATCCTCCAG CACAGCCTAC 240  
20 ATGCAGCTCA GCAGCCTGAC ATCTGAAGAC TCTGCGGTCT ATTTCTGTGC AAGAGTG 297

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

25 CTGGGGCACA GGGACCACGG TCACCGTCTC C 31

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAGGCTTATC TACAGCAGTC TGGGGCTGAG CTGGTGAGGC CTGGGGCCTC AGTGAAGATG 60  
TCCTGCAAGG CTTCTGGCTA CACATTTACC AGTTACAATA TGCACTGGGT AAAGCAGACA 120  
CCTAGACAGG GCCTGGAATG GATTGGAGCT ATTTATCCAG GAAATGGTGA TACTTCCTAC 180  
AATCAGAAGT TCAAGGGCAA GGCCCACTG ACTGTAGACA AATCCTCCAG CACAGCCTAC 240  
10 ATGCAGCTCA GCAGCCTGAC ATCTGAAGAC TCTGCGGTCT ATTTCTGTGC AAGAGTG 297

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTGGGGCACA GGGACCACGG TCACCGTCTC 30

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AGGTCCAGCT GCAGCAGTCT GGACCTGAGC TGGTAAAGCC TGGGGCTTCA GTGAAGATAT 60  
CCTGCAAGGC TTCTGGATAC ACATTCCTG ACTACTACAT GCACTGGGTG AAGCAGAAGC 120  
CTGGGCAGGG CCTTGAGTGG ATTGGAGAGA TTTATCCTGG AAGTGTAAT ACTTACTACA 180  
25 ATGAGAAGTT CAAGGGYAAG GCCTCACTGA CTGCAGACAA ATCCTCCAGC ACAGCCTACA 240  
TGCAGCTCAG CAGCCTGACA TCTGAGGACT CTGCAGTCTA TTTCTGTGCA AGACGTTACT 300

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

5 TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA 46

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

10 CAGGTTTCAGC TCCAGCAGTC TGGGGCTGAG CTGGCAAGAC CTGGGGCTTC AGTGAAGTTG 60

15 TCCTGCAAGG CTTCTGGCTA CACCTTTACT AGCTACTGGA TGCAGTGGGT AAAACAGAGG 120

CCTGGACAGG GTCTGGAATG GATTGGGGCT ATTTATCCTG GAGATGGTGA TACTAGGTAC 180

ACTCAGAAGT TCAAGGGCAA GGCCACATTG ACTGCAGATA AATCCTCCAG CACAGCCTAC 240

ATGCAACTCA GCAGCTTGGC ATCTGAGGAC TCTGCGGTCT ATTACTGTGC AAGAG 295

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

20 TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA 46

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CAGGTTTCAGC TCCAGCAGTC TGGGGCTGAG CTGGCAAGAC CTGGGGCTTC AGTGAAGTTG 60  
TCCTGCAAGG CTTCTGGCTA CACCTTTACT AGCTACTGGA TGCAGTGGGT AAAACAGAGG 120  
CCTGGACAGG GTCTGGAATG GATTGGGGCT ATTTATCCTG GAGATGGTGA TACTAGGTAC 180  
ACTCAGAAGT TCAAGGGCAA GGCCACATTG ACTGCAGATA AATCCTCCAG CACAGCCTAC 240  
ATGCAACTCA GCAGCTTGGC ATCTGAGGAC TCTGCGGTCT ATTACTGTGC AAGA 294

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA 46

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAGGTTTCAGC TCCAGCAGTC TGGGGCTGAG CTGGCAAGAC CTGGGGCTTC AGTGAAGTTG 60  
TCCTGCAAGG CTTCTGGCTA CACCTTTACT AGCTACTGGA TGCAGTGGGT AAAACAGAGG 120  
CCTGGACAGG GTCTGGAATG GATTGGGGCT ATTTATCCTG GAGATGGTGA TACTAGGTAC 180  
ACTCAGAAGT TCAAGGGCAA GGCCACATTG ACTGCAGATA AATCCTCCAG CACAGCCTAC 240  
ATGCAACTCA GCAGCTTGGC ATCTGAGGAC TCTGCGGTCT ATTACTGTGC AAGA 294

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA

46

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CAGGTCCAAC TGCAGCAGCC TGCTGCTGAG CTTGTGAAGC CTGGGGCCTC AGTGAAGCTG 60

TCCTGCAAGG CTTCTGGCTA CACTTTCACC AGCTACTGGA TAAACTGGGT GAAGCAGAGG 120

CCTGGACAAG GCCTTGAGTG GATTGGAAAT ATTTATCCTG GTAGTAGTAG TACTAACTAC 180

AATGAGAAGT TCAAGAGCAA GGCCCACTG ACTGTAGACA CATCCTCCAG CACAGCCTAC 240

ATGCAGCTCA GCAGCCTGAC ATCTGACGAC TCTGCGGTCT ATTATTGTGC AAGACG 296

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA

46

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "May also be the amino acid arginine(R) "

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15

(D) OTHER INFORMATION: /note= "May also be the amino acid  
glutamine(E) "

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 16

(D) OTHER INFORMATION: /note= "May also be the amino acid  
serine(S) "

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(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 19

(D) OTHER INFORMATION: /note= "May also be the amino acid  
proline(P) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr  
1 5 10 15

Arg Pro Ala Pro  
20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 12

(D) OTHER INFORMATION: /note= "May also be the amino acid  
arginine(R) "

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 18

(D) OTHER INFORMATION: /note= "May also be the amino acid  
glutamine(E) "

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 19

(D) OTHER INFORMATION: /note= "May also be the amino acid  
serine(S) "

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 22

(D) OTHER INFORMATION: /note= "May also be the amino acid



proline(P) "

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 2

(D) OTHER INFORMATION: /note= "May also be the amino acid

proline(P) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala  
1 5 10 15

Pro Asp Thr Arg Pro Ala Pro  
20

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: misc\_difference

(B) LOCATION: replace(30, "")

(D) OTHER INFORMATION: /note= "N represents the nucleotide

Inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CCCAAGCTTC CAGGGRCCAR KGGATARACN GRTGG

35

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGGAATTCAT GRAATGSASC TGGGTYWTYC TCTT

34

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TAATACGACT CACTATAGGG

20

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GTTTTCCCAG TCACGACGT

19

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ACTAGTCCAC ATGAGGRCCC CTGCTCAGWT TYTTGGNWTC TT

42

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCCAAGCTTA CTGGATGGTG GGAAGATGGA

30

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(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CAGATGGAAG GGCCCAAC

18

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GATTGATGCA TATCATTACC

20

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GTTATCGATG TCGAATAGCC

20

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TTGCTGCAGA TTGAGTACTG TTCT

24

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 amino acids

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(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser  
 1 5 10

5 (2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly  
 1 5 10 15

Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp Ile Gly Ser Ser  
 20 25 30

Leu Asn Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile Lys Arg Leu Ile  
 35 40 45

Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly  
 50 55 60

Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser  
 65 70 75 80

Gly Asp Phe Val Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Ser Pro Tyr  
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
 100 105

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 1 5 10 15

08766350-121296

*Sub*  
*at*  
 10

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Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
20 25 30  
Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile  
35 40 45  
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Asn Tyr Asn Gln Lys Phe  
50 55 60  
Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr  
65 70 75 80  
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
85 90 95  
Ala Arg Gly Xaa Xaa Xaa Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr  
100 105 110  
Ser Val Thr Val Ser Ser  
115

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 1..4
- (D) OTHER INFORMATION: /note= "position 54-57 of 11D10 comparison sequence #8 (Fig. 26B)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ser Asp Ser Tyr  
1

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 1..9
- (D) OTHER INFORMATION: /note= "positions 118-126 of 11D10 comparison sequence #2 and positions 100-108 of 11D10 comparison sequence #8 (Fig. 26B)"

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sequence #6 (Fig. 26B)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:51:

5.

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 1..7
- (D) OTHER INFORMATION: /note= "positions 99-105 of 11D10 comparison sequence #3 and #8 (Fig. 26B)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 1..4
- (D) OTHER INFORMATION: /note= "positions 100-103 of 11D10 comparison sequence #12 (Fig. 26B)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Val Tyr Tyr Tyr  
1

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 1..4
- (D) OTHER INFORMATION: /note= "positions 100-103 of 11D10 comparison sequence #14 (Fig. 26B)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Phe Tyr Phe Tyr  
1

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 1..4
- (D) OTHER INFORMATION: /note= "positions 100-103 of 11D10 comparison sequence #15 (Fig. 26B)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Gly Leu Phe Thr  
1

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gly Ser Thr Ala Pro Pro Ala His Arg Val Thr Ser Ala Pro Glu Ser  
1 5 10 15

Arg Pro Pro Pro  
20

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Pro Pro Pro Arg Ser Glu Pro Ala Ser Thr Val Arg His Ala Pro Pro  
1 5 10 15  
Ala Thr Ser Gly  
20

5 (2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ala Pro Asp Thr Arg Pro Pro Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 145 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met Gly Thr Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Leu Phe Pro  
1 5 10 15  
Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser  
20 25 30  
Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp  
35 40 45  
Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile  
50 55 60  
Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys  
65 70 75 80  
Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser  
85 90 95  
Ser Leu Glu Ser Gly Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala  
100 105 110



Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg  
115 120 125

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys Leu  
130 135 140

Gly  
145

5  
Sub  
Amended

10

15

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